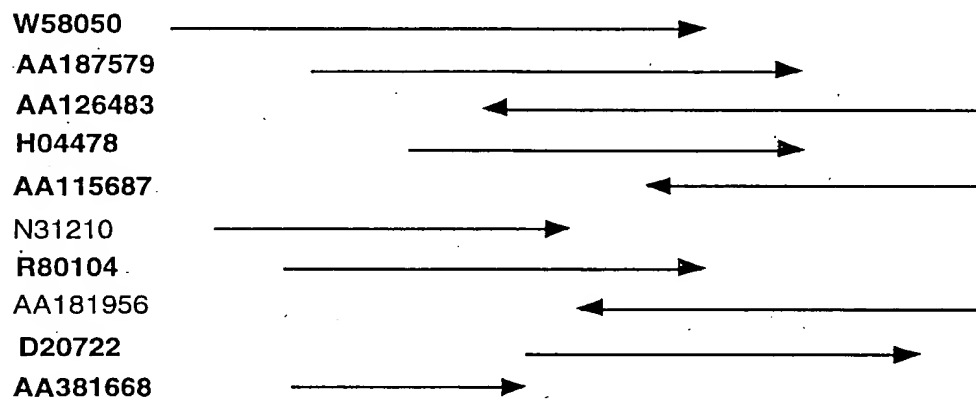
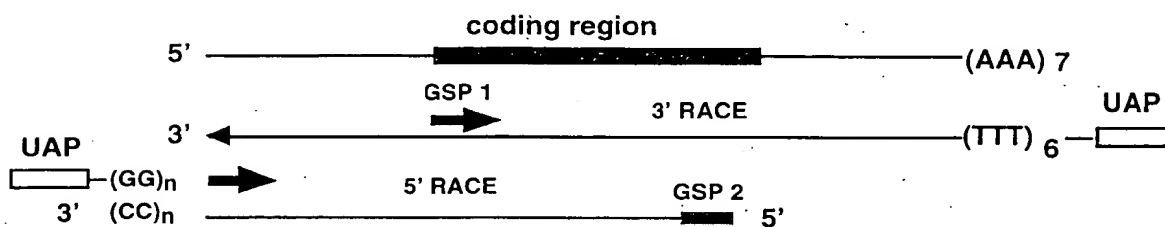


Fig. 1A

1 GCTACCTCCA ACTGCTGAGG AACCGGTTGC CTAAAGGAG CCGCAAAAG  
 51 CGCCTACGTG GAGTCCAGAG GAGCGAAGT AGTCAGATT GACTGAGAGC  
 101 CGTAAAGCGC GGCTGGCTCT CGTTTCCGG ATAACGACTA CAGCTCCGAC  
 151 TGTCAAGTCC GGCCTTCCCTC GTGTGAGGG ATCTGCCGA CCCCTGCAAA  
 201 TTCAATTCTT TTCCCATTC GGGCCCTTCC CTATCGTCG CCCCTTCACC  
 251 TTGGATCATG TTCAAGAAAT TTGATGAAA AGAAAATGTG TCCAACGTCA  
 301 TCCAGTTGAA AACTTCAGTT ATTAAGGTA TTAAGAAATCA ATTGATAGAG  
 351 CAATTTCAG GTATTGAACC ATGGCTTAAT CAAATCATGC CTAAGAAAGA  
 401 TCCTGTCAA ATAGTCCGAT GCCATGAACA TATAGAAATC CTTACAGTAA  
 451 ATGGAGAATT ACTCTTTTT AGACAAAGAG AAGGCCCTT TTATCCAACC  
 501 CTAAGATTAC TTCACAAATA TCCTTTTATC CTGCCACACC AGCAGGTTGA  
 551 TAAAGGAGCC ATCAAATTG TACTCAGTGG AGCAAATATC ATGTGTCCCA  
 601 GGCTTAACCT CTCCTGGAGC TAAGCTTTAC CCTGCTGCAG TAGATACCAT  
 651 TGTGTCTATC ATGGCAGAAG GAAAACAGCA TGCTCTATGT GTTGGAGTCA  
 701 TGAAGATGTC TGCAGAAGAC ATTGAGAAAG TCAACAAAGG AATTGGCATT  
 751 GAAAATATCC ATTATTAAA TGATGGGCTG TGGCATATGA AGACATATAA  
 801 ATGAGCCTCA GAAGGAATGC ACTTGGGCTA AATATGGATA TTGTGCTGTA  
 851 TCTGTGTTG TGTCTGTGTG TGACAGCATG AAGATAATGC CTGTGTTAT  
 901 GCTGAATAAA TTCACCAGAT GCTAAAAAAA AAAAAAAA AAAA

Fig. 1B

1 M F K K F D E K E N V S N C I Q L K T S V I K G I K N  
 28 Q L I E Q F P G I E P W L N Q I M P K K D P V K I V R  
 55 C H E H I E I L T V N G E L L F F R Q R E G P F Y P T  
 82 L R L L H K Y P F I L P H Q Q V D K G A I K F V L S G  
 109 A N I M C P R L N F S W S



**Fig. 2**



MCT-1  
8 KENVSNCIQLKTSVIKIGIKNQLIEQFPGIEWLNQIMPKDPVK 51  
||| |: :. | .: | |::: | :: |  
Cyclin H 239 KEN.RTCLSQLLDIMKSMRN.LVKKYE..PPRSEEVAVLKQ..K277

MCT-1 52IVRCHEHIEILTVN 65  
Cyclin H 278LERCHS.AE.LALN<sup>288</sup>

**Fig. 4**

Fig. 5A

1 GCTACCTCCA ACTGCTGAGG AACCGGTTGC CTAAAAGGAG CCGGCAAAAG  
51 CGCCTACGTG GAGTCCAGAG GAGCGGAAGT AGTCAGATTG GACTGAGAGC  
101 CGTAAAGCGC GGTGGCTCT CGTTTCCGG ATAACGACTA CAGCTCCGAC  
151 TGTCAGTGCC GGCCTTCCCTC GTGTGAGGG ATCTGCCGGA CCCCTGCAAA  
201 TTCAATTCTT TTCCCATTCG GGGCCCTTCC CTATCGTCGC CCCCTTCACC  
251 TTGGATC**ATG** TTCAAGAAAT TTGATGAAAA AGAAAATGTG TCCAACTGCA  
301 TCCAGTTGAA AACTTCAGTT ATTAAGGTA TTAAGAATCA ATTGATAGAG  
351 CAATTTCCAG GTATTGAACC ATGGCTTAAT CAAATCATGC CTAAGAAAGA  
401 TCCTGTCAAA ATAGTCCGAT GCCATGAACA TATAGAAATC CTTACAGTAA  
451 ATGGAGAATT ACTCTTTTTC AGACAAAGAG AAGGGCCTTT TTATCCAAACC  
501 CTAAGATTAC TTCACAAATA TCCTTTTATC CTGCCACACC AGCAGGTTGA  
551 TAAAGGAGCC ATCAAATTG TACTCAGTG AGCAAATATC ATGTGTCCAG  
601 GCTTAACTC TCCTGGAGCT AAGCTTTACC CTGCTGCAGT AGATACCATT  
651 GTTGCTATCA TGGCAGAAGG AAAACAGCAT GCTCTATGTG TTGGAGTCAT  
701 GAAGATGTCT GCAGAAGACA TTGAGAAAGT CAACAAAGGA ATTGGCATTG  
751 AAAATATCCA TTATTTAAAT GATGGGCTGT GGCATATGAA GACATATAAA  
801 **TGAG**CCCTCAG AAGGAATGCA CTGGGGCTAA ATATGGATAT TGTGCTGTAT  
851 CTGTGTTTGT GTCTGTGTGT GACAGCATGA AGATAATGCC TGTGGTTATG  
901 CTGAATAAAT TCACCAGATG CTAAAAAAA AAAA

Fig. 5B

1 M F K K F D E K E N V S N C I Q L K T S V I K G I K N  
28 Q L I E Q F P G I E P W L N Q I M P K K D P V K I V R  
55 C H E H I E I L T V N G E L L F F R Q R E G P F Y P T  
82 L R L L H K Y P F I L P H Q Q V D K G A I K F V L S G  
109 A N I M C P G L T S P G A K L Y P A A V D T I V A I M  
136 A E G K Q H A L C V G V M K M S A E D I E K V N K G I  
163 G I E N I H Y L L N D G L W H M K T Y K